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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/981,566A

DATE: 04/23/2002

TIME: 10:33:02

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Output Set: N:\CRF3\04232002\1981566A.raw

- 3 <110> APPLICANT: Kekuda et al.
- 5 <120> TITLE OF INVENTION: Novel GPCR-like Proteins and Nucleic Acids Encoding
- Same
- 8 <130> FILE REFERENCE: 21402-163
- 10 <140> CURRENT APPLICATION NUMBER: 09/981,566A
- 11 <141> CURRENT FILING DATE: 2001-10-16
- 13 <150> PRIOR APPLICATION NUMBER: 60/240,704
- 14 <151> PRIOR FILING DATE: 2000-10-16
- 16 <150> PRIOR APPLICATION NUMBER: 60/262,159
- 17 <151> PRIOR FILING DATE: 2001-01-17
- 19 <150> PRIOR APPLICATION NUMBER: 60/263,340
- 20 <151> PRIOR FILING DATE: 2001-01-22
- 22 <150> PRIOR APPLICATION NUMBER: 60/264,118
- 23 <151> PRIOR FILING DATE: 2001-01-25
- 25 <150> PRIOR APPLICATION NUMBER: 60/308,203
- 26 <151> PRIOR FILING DATE: 2001-07-27
- 28 <150> PRIOR APPLICATION NUMBER: 60/243,497
- 29 <151> PRIOR FILING DATE: 2000-10-26
- 31 <150> PRIOR APPLICATION NUMBER: 60/244,542
- 32 <151> PRIOR FILING DATE: 2000-10-31
- 34 <150> PRIOR APPLICATION NUMBER: 60/269,031
- 35 <151> PRIOR FILING DATE: 2001-02-15
- 37 <150> PRIOR APPLICATION NUMBER: 60/245,484
- 38 <151> PRIOR FILING DATE: 2000-11-03
- 40 <150> PRIOR APPLICATION NUMBER: 60/255,017
- 41 <151> PRIOR FILING DATE: 2000-12-12
- 43 <150> PRIOR APPLICATION NUMBER: 60/263,216
- 44 <151> PRIOR FILING DATE: 2001-01-22
- 46 <150> PRIOR APPLICATION NUMBER: 60/268,225
- 47 <151> PRIOR FILING DATE: 2001-02-12
- 49 <160> NUMBER OF SEQ ID NOS: 209
- 51 <170> SOFTWARE: PatentIn Ver. 2.1
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- 55 <212> TYPE: DNA
- 56 <213> ORGANISM: Homo sapiens
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- 61 ctcgccttca tgggaaacac catcatcata gttatggtca tagctgacac ccacctacat 180
- 62 acacccatgt acttetteet gggcaatttt teeetgetgg agatettggt aaccatgaet 240
- 63 geagtgeeca ggatgetete agacetgttg gteececaea aagteattae etteaetgge 300
- 64 tgcatggtcc agttctactt ccacttttcc ctggggtcca cctccttcct catcctgaca 360

Input Set : A:\Cura-461.app

Output Set: N:\CRF3\04232002\I981566A.raw

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66 agccqqqcta tqtqtqtcca qctqqctqqq qctqcctqqq cagctccttt cctagccatg 480
67 qtacccactg tecteteeeg ageteatett gattactgee atggegaegt cateaaceae 540
68 ttcttctgtg acaatgaacc tctcctgcag ttgtcatgct ctgacactcg cctgttggaa 600
69 ttotgggact ttotgatggo ottgacettt gtoctoagot cottootggt gaccotoato 660
70 tectatgget acatagtgae caetgtgetg eggateeeet etgeeageag etgeeagaag 720
71 gettteteca ettgegggte teaceteaca etggtettea teggetacag tagtaceate 780
72 tttctgtatg tcaggcctgg caaagctcac tctgtgcaag tcaggaaggt cgtggccttg 840
73 gtgacttcag ttctcaccc ctttctcaat ccctttatcc ttaccttctg caatcagaca 900
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90 Tyr Leu Leu Ala Phe Met Gly Asn Thr Ile Ile Ile Val Met Val Ile
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                                40
93 Ala Asp Thr His Leu His Thr Pro Met Tyr Phe Phe Leu Gly Asn Phe
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                            55
96 Ser Leu Leu Glu Ile Leu Val Thr Met Thr Ala Val Pro Arg Met Leu
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                        70
99 Ser Asp Leu Leu Val Pro His Lys Val Ile Thr Phe Thr Gly Cys Met
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                                         90
102 Val Gln Phe Tyr Phe His Phe Ser Leu Gly Ser Thr Ser Phe Leu Ile
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103
                100
105 Leu Thr Asp Met Ala Leu Asp Arg Phe Val Ala Ile Cys His Pro Leu
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                                120
                                                    125
108 Arg Tyr Gly Thr Leu Met Ser Arg Ala Met Cys Val Gln Leu Ala Gly
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                            135
111 Ala Ala Trp Ala Ala Pro Phe Leu Ala Met Val Pro Thr Val Leu Ser
                                            155
                        150
114 Arg Ala His Leu Asp Tyr Cys His Gly Asp Val Ile Asn His Phe Phe
115
                    165
                                        170
117 Cys Asp Asn Glu Pro Leu Leu Gln Leu Ser Cys Ser Asp Thr Arg Leu
118
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                                    185
120 Leu Glu Phe Trp Asp Phe Leu Met Ala Leu Thr Phe Val Leu Ser Ser
                                200
           195
123 Phe Leu Val Thr Leu Ile Ser Tyr Gly Tyr Ile Val Thr Thr Val Leu
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                            215
                                                220
126 Arg Ile Pro Ser Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly
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127 225
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129 Ser His Leu Thr Leu Val Phe Ile Gly Tyr Ser Ser Thr Ile Phe Leu
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132 Tyr Val Arg Pro Gly Lys Ala His Ser Val Gln Val Arg Lys Val Val
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Input Set : A:\Cura-461.app

Output Set: N:\CRF3\04232002\I981566A.raw

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136 275
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150 <400> SEQUENCE: 3
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152 taggettete etectttagt gagetaeaga ceettetata taggeceette eteatgettt 120
153 atcttctcgc cttcatggga aacaccatca tcatagttat ggtcatagct gacacccacc 180
154 tacatacacc catgtacttc ttcctgggca atttttccct gctggagatc ttggtaacca 240
155 tgactgcagt gcccaggatg ctctcagacc tgttggtccc ccacaaagtc attaccttca 300
156 etggetgeat ggtecagtte tacttecact tttecetggg gtecacetee tteeteatee 360
157 tgacagacat ggcccttgat cgctttgtgg ccatctgcca cccactgcgc tatggcactc 420
158 tgatgagccg ggctatgtgt gtccagctgg ctggggctgc ctggggcagct cctttcctag 480
159 ccatggtacc cactgtcctc tecegagete atettgatta etgecatgge gaegteatea 540
160 accaettett etgtgacaat gaacetetee tgeagttgte atgetetgae actegeetgt 600
161 tagaatteta agacttteta atagaecatga cetttateet eageteette etagatgaece 660
162 tcatctcata tggctacata gtgaccactg tgctgcggat cccctctgcc agcagctgcc 720
163 agaaggettt etecaettge gggteteaec teaeaetggt etteategge taeagtagta 780
164 ccatctttct gtatgtcagg cctggcaaag ctcactctgt gcaagtcagg aaggtcgtgg 840
165 ccttggtgac ttcagttctc acccctttc tcaatccctt tatccttacc ttctgcaatc 900
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182 Leu Ala Phe Met Gly Asn Thr Ile Ile Ile Val Met Val Ile Ala Asp
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185 Thr His Leu His Thr Pro Met Tyr Phe Phe Leu Gly Asn Phe Ser Leu
188 Leu Glu Ile Leu Val Thr Met Thr Ala Val Pro Arg Met Leu Ser Asp
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                         70
189 65
191 Leu Leu Val Pro His Lys Val Ile Thr Phe Thr Gly Cys Met Val Gln
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194 Phe Tyr Phe His Phe Ser Leu Gly Ser Thr Ser Phe Leu Ile Leu Thr
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197 Asp Met Ala Leu Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg Tyr
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Input Set : A:\Cura-461.app

Output Set: N:\CRF3\04232002\I981566A.raw

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203 Trp Ala Ala Pro Phe Leu Ala Met Val Pro Thr Val Leu Ser Arg Ala
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206 His Leu Asp Tyr Cys His Gly Asp Val Ile Asn His Phe Phe Cys Asp
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                                        170
                                                             175
209 Asn Glu Pro Leu Leu Gln Leu Ser Cys Ser Asp Thr Arg Leu Leu Glu
210
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                                    185
212 Phe Trp Asp Phe Leu Met Ala Met Thr Phe Val Leu Ser Ser Phe Leu
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                                200
                                                     205
215 Val Thr Leu Ile Ser Tyr Gly Tyr Ile Val Thr Thr Val Leu Arg Ile
                            215
                                                220
218 Pro Ser Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly Ser His
219 225
                        230
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221 Leu Thr Leu Val Phe Ile Gly Tyr Ser Ser Thr Ile Phe Leu Tyr Val
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224 Arg Pro Gly Lys Ala His Ser Val Gln Val Arg Lys Val Val Ala Leu
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                                    265
227 Val Thr Ser Val Leu Thr Pro Phe Leu Asn Pro Phe Ile Leu Thr Phe
228
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230 Cys Asn Gln Thr Val Lys Thr Val Leu Gln Gly Gln Met Gln Arg Leu
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233 Lys Gly Leu Cys Lys Ala Gln
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245 atettetege etteatggga aacaceatea teatagttat ggteataget gacacecace 180
246 tacatacace catgtaette tteetgggea attttteeet getggagate ttggtaacea 240
247 tgactgcagt gcccaggatg ctctcagacc tgttggtccc ccacaaagtc attaccttca 300
248 ctggctgcat ggtccagttc tacttccact tttccctggg gtccacctcc ttcctcatcc 360
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252 accaettett etgtgacaat gaacetetee tgeagttgte atgetetgae actegeetgt 600
253 tggaattetg ggaetttetg atggeettga cetttgteet eageteette etggtgaeee 660
254 teateteeta tggetacata gtgaceaetg tgetgeggat eecetetgee ageagetgee 720
255 agaaggettt etecaettge gggteteaee teaeaetggt etteategge taeagtagta 780
256 ccatctttct gtatgtcagg cctggcaaag ctcactctgt gcaagtcagg aaggtcgtgg 840
257 cettggtgae tteagttete acceeettte teaateeett tateettaee ttetgeaate 900
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259 aatgatgagc c
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263 <211> LENGTH: 311
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Input Set : A:\Cura-461.app

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265 <213> ORGANISM: Homo sapiens
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272
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                                     25
274 Leu Ala Phe Met Gly Asn Thr Ile Ile Ile Val Met Val Ile Ala Asp
275
            35
                                 40
277 Thr His Leu His Thr Pro Met Tyr Phe Phe Leu Gly Asn Phe Ser Leu
                             55
280 Leu Glu Ile Leu Val Thr Met Thr Ala Val Pro Arg Met Leu Ser Asp
281 65
                         70
                                              75
283 Leu Leu Val Pro His Lys Val Ile Thr Phe Thr Gly Cys Met Val Gln
                     85
                                         90
286 Phe Tyr Phe His Phe Ser Leu Gly Ser Thr Ser Phe Leu Ile Leu Thr
287
                100
                                    105
289 Asp Met Ala Leu Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg Tyr
                                120
292 Gly Thr Leu Met Ser Arg Ala Met Cys Val Gln Leu Ala Gly Ala Ala
        130
                            135
295 Trp Ala Ala Pro Phe Leu Ala Met Val Pro Thr Val Leu Ser Arg Ala
296 145
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                                             155
298 His Leu Asp Tyr Cys His Gly Asp Val Ile Asn His Phe Phe Cys Asp
299
                    165
                                        170
301 Asn Glu Pro Leu Leu Gln Leu Ser Cys Ser Asp Thr Arg Leu Leu Glu
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                                    185
304 Phe Trp Asp Phe Leu Met Ala Leu Thr Phe Val Leu Ser Ser Phe Leu
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                                                     205
           195
307 Val Thr Leu Ile Ser Tyr Gly Tyr Ile Val Thr Thr Val Leu Arg Ile
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                            215
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310 Pro Ser Ala Ser Ser Cys Gln Lys Ala Phe Ser Thr Cys Gly Ser His
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313 Leu Thr Leu Val Phe Ile Gly Tyr Ser Ser Thr Ile Phe Leu Tyr Val
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                                        250
316 Arg Pro Gly Lys Ala His Ser Val Gln Val Arg Lys Val Val Ala Leu
317
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                                    265
                                                         270
319 Val Thr Ser Val Leu Thr Pro Phe Leu Asn Pro Phe Ile Leu Thr Phe
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Use of many to a problem been detected in the Securence Listing Review the Secretice Listing to ensure a particular inglexplanation is present in the K220X to K220X treds of each sequence using mor Xda.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/981,566A

DATE: 04/23/2002 TIME: 10:33:03

Input Set : A:\Cura-461.app

Output Set: N:\CRF3\04232002\I981566A.raw

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